Figure 1A

IgG1 library

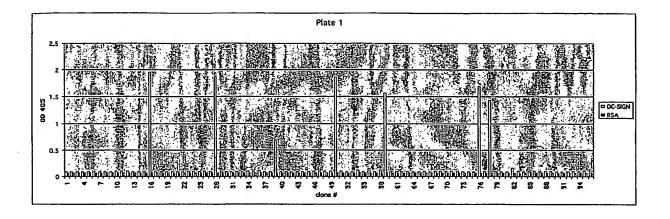
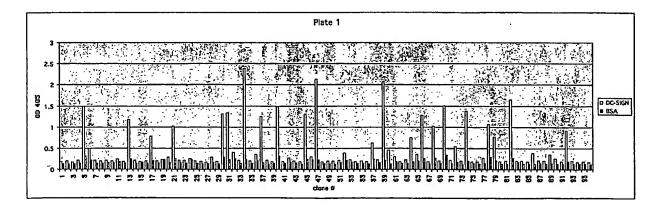


Figure 1B

IgG2a library



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Figure 2

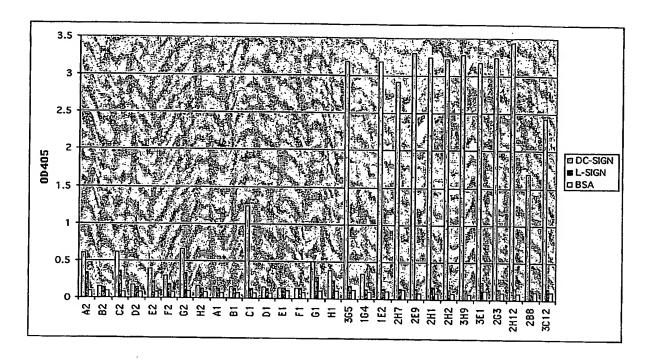
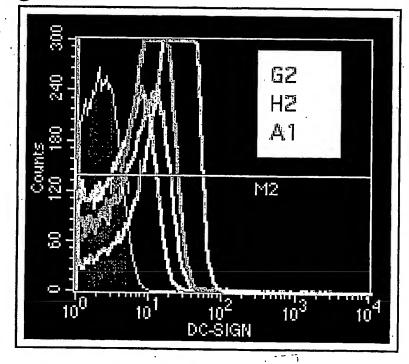


Figure 3



A1= clone 1 H2=clone 15 G2=clone 16

Figure 4a

Light chain sequences

DIQMTQTTSSLSASLGDRVTITCRASQDINNYLNWYQQKP Majority 10 20 _______ 1 DIQMTQSPASLSASVGETITITCRASENIHNYLAWYQQNQ 1G4LC 1 DIQMTQTTSSLSASLGDRVTITCRTSQDIDNYLNWYQQKP 2B8LC DIPMTQTTSSQSASLGDRVTITCRASQDINNYLNWYQQKP 2H1LC DIQMTQTTSSLSASLGDRVTISCRASHDINDYLNWYQQKP DIQMTQTTSSLSASLGDRVTITCRASQDISNYLNWYQQKP 1 DIQMTQTTSSQSASLGDRVTITCRASQDINNYLNWYQQKP 1 DIQMTQTTSSLFASLGDRVTISCRASQDIRNNLNWYQQKP 1 DIQMTQTTSSLSASLGDRVTISCRASHDINDYLNWYQQKP 3H9LC D G T V K L L I Y Y T S R L H S G V P S R F S G S G S G T D Ý S L T I S N L A Q Majority 41 GKSPQLLVYNAKTLAVGVPSRFSGSGSGTQFSLKIVSLQP 1G4LC 41 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLAQ 2B8LC DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQ 2H1LC DGTVKLLIYYTSSLQSGVPSRFRGYGSGTDYSLTISNLAQ 2H2LC DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLAQ 41 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQ 3E1LC DGTVKLLIYYTSSLPSGVPSRFSGSRSGTDYSLTISNLEQ 3E7LC DGTVKLLIYYTSSLQSGVPSRFRGYGSGTDYSLTISNLAQ 3H9LC EDIATYFCQQGDTLPWTFGGGTKLEIKRA (SEQ ID NO: 9) Majority 81 EDFGNYYCQHFWNTPWTFGRGTKLEIKRA (SEQ ID NO: 10) 1G4LC 81 EDIATYFCQQGDTLPFTFGSGTTLEIKRA (SEQ ID NO: 11) 2B8LC 81 EDLVTYFCQQGKTLPWTFGGGTKLEIKRA (SEQ ID NO: 12) 2H1LC 81 EDFATYFCQQGHTLPYTFGGGTKLEIKRA (SEQ ID NO: 13) EDIATYFCQQGDKLPFTFGSGTTLEIKRA (SEQ ID NO: 14) 3C12LC 81 E D L A T Y F C Q Q G K T L P W T F G G G T K L E I K R A (SEQ ID NO: 15)
81 E D I A T Y F C Q Q G D T L P P T F G G G T K L E I K R A (SEQ ID NO: 16)
81 E D F A T Y F C Q Q G H T L P Y T F G G G T K L E I K R A (SEQ ID NO: 17) 3E1LC 3E7LC 3H9LC

1__ 1

Figure 4 b

Heavy chain sequences

```
EVQLQQSGPELVKPGASVKISCKASGYSFT-GYYMHWVKQ Majority
10 20 30 40
                                            --+----
                            --+----
EVQLQQSGPGLVKPSQSLSLACSVTGYSITSGYYWNWIRQ 1G4HC
EVQLQQSGPELVKPGASVKISCKASGYSFT-GYYMHWVKQ 1H2HC
EVQLQQSGPELVKPGASVKISCKASGYSFT-GYYMHWVKQ 2B8HC
E V Q L Q Q S G P E L V K P G T S V K I S C K A S G Y S F T - G Y Y I H W V R Q
                                                                2H1HC
EVQLQQSGPELVKPGTSVKISCKASGYSFT-GYYIHWVRQ
                                                                2H2HC
E V Q L Q Q S G P E L V K P G A S V K I S C K A S G Y S F T - G Y Y M H W V K Q
                                                                3C12HC
EVQLQQSGPELVKPGASVKISCKASGYSFT-GYYMHWVKQ 3E1HC
EVQLQQSGAELVRPGALVKLSCKASGFNIK-DYYIHWVKQ 3E7HC
SHVKSLEWIGRINPYNGATSYNQNFKDKASLTVDKSSTTV Majority
   50 60 70
                                            __+____
                                                            --+-
SPGNKLEWMGYISYD-GNSDYNPSFKNRISITRDTSKNQF 1G4HC
S H V K S L E W I G R I N P Y N G A T S Y N Q N F K D K A S L T V D K S S T T V 1H2HC
S H V K S L E W I G R I N P Y N G A T Y Y N H N F K D K A T L T V H K S S T T V 2B8HC
RHVKSLEWIGRINPYSGATSYNQSFKDKASLTVDKSSTTA
RHVKSLEWIGRINPYSGATSYNQSFKDKASLTVDKSSTTA
S H V K S L E W I G R I N P Y N G A T S Y N Q N F K D K A S L T V D K S S T T V
                                                                3C12HC
SHVKSLEWIGRINPYNGAPSYNQNFKDKASLTVDESSTTV 3E1HC
RPEQGLEWIGWIDPENGNTIYDPKFQGKASITADTSSNTA 3E7HC
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V Majority
90 100 110
                                                             120
                             __+____
FLRLNSLTTEDTATYYCVRDDSGR--FPQWGQGTLVTVSA 1G4HC (SEQ
ID NO: 18)
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G S S V A V 1H2HC
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V
                                                                2B8HC
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V
                                                                2H1HC
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V
                                                                2H2HC
                                                                3C12HC
Y M E V H S L T S E D S A V Y Y C V R S N D G Y Y S Y P M D Y W G Q G T S V T V
                                                                3E1HC
Y L Q L S S L T S E D T A V Y Y C A R Y Y L G - - - - V D Y W G Q G T S V T V 3E7HC
                                                                Majority
S S (SEQ ID NO: 19)
      (SEQ ID NO: 20) 1H2HC
s s
      (SEQ ID NO: 21) 2B8HC
SS
      (SEQ ID NO: 22) 2H1HC
      (SEQ ID NO: 23) 2H2HC
      (SEQ ID NO: 24) 3C12HC
 s s
     (SEQ ID NO: 25) 3E1HC
 s s
      (SEQ ID NO: 26) 3E7HC
```

1 1

Figure 4c

			-				
IgG2a library Heavy Chains	CDR1		CDR2	0	CDR3		
EVQLQQSGPDLVKPGASVRISCKTSGFTFA	NYYIH	WVKQRPGQGLEWIG	NYXIH WVKQRPGQGLEWIG WIFPGNEKTEYNEKFKG KATLTADKSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY	QLSSLTSEDSAVYFCARG	KGYAVDY	WGQGTSVTVSSAKTT	т
ASVKLSCTASGEN	DIYMH	WVKQRPEQGLEWIG	IK <i>DIYMH</i> WVKQRPEQGLEWIG R <i>IDPANGNIKYDPKEQG K</i> ATITADISSNTAYLQLSSLTSEDTAVYYCARD YYGIYVDX	QLSSLTSEDTAVYYCARD)	YGIYVDY	WGQGTTLTVSSAK	7
(SEQ ID NO: 28) EVQLQQSGAELARPGASVKLSCKASGYTFR	SYMMO	WVKQRPGQGLEWIG	SYMMQ WVKQRPGQGLEWIG AIYPGDGDTRYITQKFKG KATLITADKSSSTAYMQLSSLASEDSAVYFCARG GLKSFYAMDHWGQGTSVTVSSAK	QLSSLASEDSAVYFCARG (SLKSFYAMD		ო
(SEQ ID NO: 29) EVQLQQSGPDLVKPGASVRISCKTSGFTFA	SYYIH	WVKQRPGQGLEWIG	SYXIH WVKQRPGQGLEWIG WIFPGNEKTEXNEKEKG KATLTADRSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY	QLSSLTSEDSAVYFCARG)	rGYAVDY	WGQGTSVTVSSAKT	4
(SEQ ID NO: 30) EVQLQQSGPDLVKPGASVRISCKASGFTFA		WVKQRPGQGLEWIG	SYXIH WVKQRPGQGLEWIG WIFPGNNNTKSNEKFKG KATLTADKSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY	QLSSLTSEDSAVYECARG	<i>YGYAVDY</i>	WGQGTSVTVS	S
(SEQ ID NO: 31) EVQLQQSGPDLVKPGASVRISCKASGFTFA		WVKQRPGQGLEWIG	SYXIH WVKQRPGQGLEWIG WIFFGNNNIKSNEKFKG KATLTADKSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY	QLSSLTSEDSAVYECARG	rgxavdx	WGQGISVTVSSAKT 7	
(SEQ ID NO: 32) EVQLQQSGAELVKPGASVKLSCTASDENIK	DIXIO	WVKQRPEQGLEWVG	(SEQ ID NO: 32) EVOLQOSGAELVKFGASVKLSCTASDENIK <i>DIYIQ</i> WVKQRPEGGLEWVG R <i>IDPANGEIKYDPKFQG</i> KATITADTSSNTAYLQLSSLTSEDTAVYYCTAY <i>FLVY</i>	QLSSLTSEDTAVYYCTAY A	FLVY	WGQGTLVTVSAAKTT	œ
(SEQ ID NO: 33) EVQLKESGPGLVAPSQSLSITCTVSGFSLS	RYTVH	WIRQPPGKGLEWLG	RYTVH WIRQPPGKGLEWLG MIWGGGTTDYNSALKS RLSISKDNSESQVFL	RLSISKDNSESQVELKMDSLQTDDTAKYYCARI NFGILGY	VFGILGY	WGQGTLVTVSAAKTT	
11(SEQ ID NO: 34) EVOLQOSGTELVRPGALVKLSCKASGFNIK 15(SEO ID NO: 35)	DYFMH	WVKORPEQGLEWIG	11(SEQ ID NO: 34) EVOLQOSGIELVRBGALVKLSCKASGENIK <i>DYFMH</i> WVKQRPEQGLEWIG WIDPKNGNIIYDEKEQV KASITADISSNIAYLQLISLISEDIAVYYCITI YPNALDY 15(SEO ID NO: 35)	QLTSLTSEDTAVYYCTT	YPNALDY	WGQGTSVTVSSAKTT	

DIVQTQSPASLAVSLGQRATISC *KASQSVDYDGDSYM*V WYQQKPGQPPKLLIY *AASNLHS GVPS*RFSGSGSGTDYSLTISNLEQADIATYFC *QQGKTLPW*T FGGGTKLEIKR 15 (SEQ 1D NO: 44) WYQQKPDGTVKLLIY YTSRLHS GVPSRESGSGSGTDYSLTISNLEQEDIATYFC QQGNTLPPT FGGGTKLEIKR 11(SEQ ID VA WYQQRPGQSPKLLIY WASTRHT GVPDRFTGSGSGTDYTLTISSVQAEDLALYYC QQYYSTPRT FGGGTKLEIKR 4(SEQ ID VA WYQQKPGQSPKLLIY SASYRYT GVPDRFTGSGSGTDFTFTISSVQAEDLAVYYC QQHYITPLT FGAGTKLELKR 1(SEQ ID DVVNIQIPLILSVIIGQPASISC KSSQSLIDSDGKIYLN WLLWRPGQSPKRLIY LVSKLDS GVPDRFIGSGSGTDFTLKISRVEAEDLGVYFC WQDIHFPHV HVRCWDQAGIT 2(SEQ ID VS WYQQKPDQSPKLLIY GSSNRST GVPDRFTGSGSATDFTLTISSVQAEDLADYHC GQSYNYPPT FGGGTKLEIKR 3(SEQ ID WYQQKPDGTVKLLLY YTSTLHS GVPSRFSGSGSTDYSLTISNLEPEDVATYYC QQYGNLPYT FGGGTKLEIKR 5(SEQ ID WYQQKPDGTVKLLIY YTSRLHS GVPSRFSGSGSTDYSLTISNLEQADIATYFC QQGKTLPWT FGGGTKLEIKR 7 (SEQ ID WYQQNPGQSIKLIIY WASTRHI GVPDRFIGSGSGTDYTLIINSVQAEDLILYYC QQHYIIPLI FGAGIKLELKR 8 (SEQ ID RYPDAQTISSLSASLGDRVIISC RASQDISNYLN NO: 43) NO: 39) RYQMTQTTSSLSASLGDRVTISC SASQDITWYLN NO: 40) DIOCTOTISSISASIGDRVIISC RASQDISNYIN RHOMTOSHKEMSTSVGDRVSITC KASQDVSTAVA DIAMTQSHKFMSTPVGDRVSITC KASQDVSTA SIVLTQSPKSMSMSVGERVTLSC KASENVGTY DIVLTQSHKFMSTSVGDRVSITC KASQDVSTA Light chains

Figure 5A IgG1 library

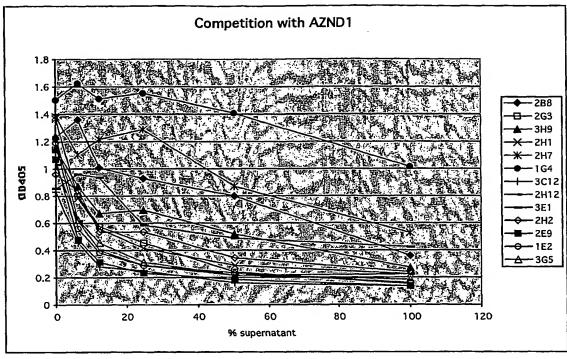
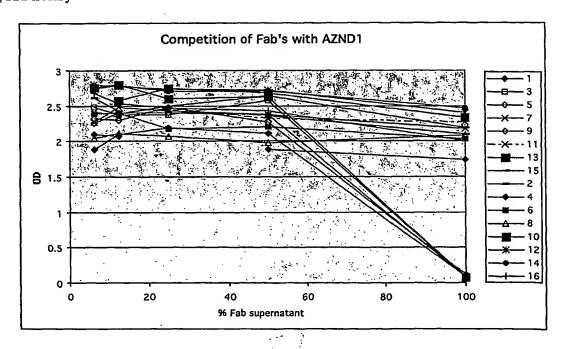


Figure 5B IgG2a library



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Figure 6

